

SEQUENCE LISTING

<110> Ford, Gregory
Bloom, Debra
Fathman, C. Garrison

<120> Anergy Associated Genes

<130> STAN177

<140> Unassigned

<141> 2001-05-11

<150> 60/203,513

<151> 2000-05-11

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<213> Mus musculus

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agagagaagc	tgatggaaat	ttttgagtcc	cattcattag	ataattgaca	tactcagttt	180
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aaacttttta	ttatcagttc	aaaatcagtt	tgttggttcag	aagaaagatt	gctaattgtat	120
gatgggaagt	gtttggccat	gcttgcttgt	tggcagttaa	gacaaatgta	acacacacac	180
acacacacac	acacacacac	acacatgaga	tgagtcactg	ccttctatgg	ccttctatgg	240
tgtacgacag	ttagagatgc					260

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ttacaaaccc	agcggctgcc	agttcaaaaa	atcaagacct	atatcatctg	ggagggggcc	180
atgagagctg	taatttttgt	caccaaacga	ggactaaaaa	tttgtgctga	tccagaaccc	240
aaatgggtga	aagcagcgat	caagactgtg	gatggcaggg	ccagtaccag	aaagaacatg	300
gctgaaactg	ttcccacagg	agcccagagg	tccaccagca	cagcagtaac	cctgactggg	360
taacagcctc	caggacaatg	tttcctcact	cgtaagcag	ctcatctcag	ttcccaaacc	420

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gtaataaata tttattattg 500

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<212> DNA
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<400> 4
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<222> (358)...(1641)

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cccgggtgga aaatcgatgg gcccgcgggc gctctagaag tactctcgag aagctttttg 180
aattcggcac gagcgcttgc ttgcaggagc tgcgtctgca gtacgctggc cgctgacgct 240
gcgtgccggc tggcagggca gcctgcgacc tcgctggccc cgcgccgct gctagccgcc 300
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ggg ccg ccg ccc ggg atc ggg gtc tac tgc cgc ggc ggc tgc gga gct 408
Gly Pro Pro Pro Gly Ile Gly Val Tyr Cys Arg Gly Gly Cys Gly Ala
5 10 15

gcc cgg cta ctg gct tgg tgc ttc ctt ctg gct ctg agt ccg cac gcg 456
Ala Arg Leu Leu Ala Trp Cys Phe Leu Leu Ala Leu Ser Pro His Ala
20 25 30

ccc ggt tcc cgg gga gcc gaa gcc gtg tgg act gcg tac ctc aac gtg 504
Pro Gly Ser Arg Gly Ala Glu Ala Val Trp Thr Ala Tyr Leu Asn Val
35 40 45

tcc tgg cgg gtt ccg cac acc gga gtg acc gca cgg tgt gga gct gag 552
Ser Trp Arg Val Pro His Thr Gly Val Thr Ala Arg Cys Gly Ala Glu
50 55 60 65

cga gag gcc gtg tac gcc cag gac tcg ccg ctg aag ccc gtc tcc ggg 600
Arg Glu Gly Val Tyr Gly Gln Asp Ser Pro Leu Lys Pro Val Ser Gly
70 75 80

gtc ctg gta ccg ccc gac ggg ccc ggg gcg ctc aac gcc tgt aac ccg 648
Val Leu Val Pro Pro Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn Pro
85 90 95

cac acc aat ttc acg gtg ccc acg gtt tgg ggg agc acg gtg caa gta His Thr Asn Phe Thr Val Pro Thr Val Trp Gly Ser Thr Val Gln Val 100 105 110	696
tct tgg ttg gcc ctc atc caa cgc ggt gga ggc tgc acc ttc gcg gac Ser Trp Leu Ala Leu Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala Asp 115 120 125	744
aag atc cat ctg gct tca gag aga ggg gct tct gga gcg gtc atc ttt Lys Ile His Leu Ala Ser Glu Arg Gly Ala Ser Gly Ala Val Ile Phe 130 135 140 145	792
aac ttc cct ggg acc cgc aat gag gtc atc ccc atg tct cac ccg ggt Asn Phe Pro Gly Thr Arg Asn Glu Val Ile Pro Met Ser His Pro Gly 150 155 160	840
gct ggg gac att gtt gca atc atg att ggc aat ctg aaa gga aca aaa Ala Gly Asp Ile Val Ala Ile Met Ile Gly Asn Leu Lys Gly Thr Lys 165 170 175	888
att ctg cag tct att caa aga ggc atc caa gtc aca atg gtc atc gaa Ile Leu Gln Ser Ile Gln Arg Gly Ile Gln Val Thr Met Val Ile Glu 180 185 190	936
gta ggg aaa aaa cat ggc cct tgg gtg aat cat tat tca att ttc ttc Val Gly Lys Lys His Gly Pro Trp Val Asn His Tyr Ser Ile Phe Phe 195 200 205	984
gtt tct gtg tcc ttt ttc ata att acg gca gca acc gtg ggc tat ttc Val Ser Val Ser Phe Phe Ile Ile Thr Ala Ala Thr Val Gly Tyr Phe 210 215 220 225	1032
atc ttt tat tct gct cga aga tta cga aat gca aga gct caa agc agg Ile Phe Tyr Ser Ala Arg Arg Leu Arg Asn Ala Arg Ala Gln Ser Arg 230 235 240	1080
aag cag agg cag tta aag gca gat gct aaa aaa gct att gga aag ctt Lys Gln Arg Gln Leu Lys Ala Asp Ala Lys Lys Ala Ile Gly Lys Leu 245 250 255	1128
cag ctg cgc acc ttg aaa caa gga gac aag gaa att ggc cct gat gga Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro Asp Gly 260 265 270	1176
gat agc tgt gct gtg tgc att gag ctc tat aag cca aat gat ttg gtg Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp Leu Val 275 280 285	1224
cgc atc cta acc tgc aat cat att ttc cat aag aca tgt gtg gac ccg Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val Asp Pro 290 295 300 305	1272
tgg ctt tta gaa cac agg act tgc ccc atg tgc aag tgt gac att ctc Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp Ile Leu 310 315 320	1320
aaa gct ctg gga att gag gtg gat gtt gaa gat gga tca gtg tct tta Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val Ser Leu	1368

325	330	335	
caa gtt cct gtt tct aat gaa gca tct aat act gcc tct ccc cat gaa			1416
Gln Val Pro Val Ser Asn Glu Ala Ser Asn Thr Ala Ser Pro His Glu			
340	345	350	
gag gac agt cgc agt gag act gca tca tct gga tat gct tca gta caa			1464
Glu Asp Ser Arg Ser Glu Thr Ala Ser Ser Gly Tyr Ala Ser Val Gln			
355	360	365	
gga gca gat gag cca cct ctg gag gaa cat gcg cag tca gca aat gaa			1512
Gly Ala Asp Glu Pro Pro Leu Glu Glu His Ala Gln Ser Ala Asn Glu			
370	375	380	385
aat cta cag ctg gta aac cat gaa gca aat tct gtg gcc gtg gat gtt			1560
Asn Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val Asp Val			
390	395	400	
gtt ccc cat gtt gac aac cca acc ttt gaa gaa gat gaa act cct gat			1608
Val Pro His Val Asp Asn Pro Thr Phe Glu Glu Asp Glu Thr Pro Asp			
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caa gag gca gct gtt cgg gag att aaa tct taa aaatctgtgt caatagaaaa			1661
Gln Glu Ala Ala Val Arg Glu Ile Lys Ser *			
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gggtaaacgt aaaacaagaa tgatactgaa agtgctgagg taacttatat tatactatag			1781
ttaaattggct taacatatatt accccagtag cgttttccac aaactcacca taacgttttt			1841
cataggcaag tttcctcttg gtgatatgta tagcaacatt tttaacattc agaaccgtct			1901
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agtgtggagt agctgtaatc actttgtttt atgatagtat cataattaaa caatactact			2021
acttttagctt gggctctgtg tgtcggggtt tgtctccagg tgcttatatt gatctggaat			2081
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Ala Pro Gly Ser Arg Gly Ala Glu Ala Val Trp Thr Ala Tyr Leu Asn			
35 40 45			
Val Ser Trp Arg Val Pro His Thr Gly Val Thr Ala Arg Cys Gly Ala			
50 55 60			
Glu Arg Glu Gly Val Tyr Gly Gln Asp Ser Pro Leu Lys Pro Val Ser			
65 70 75 80			
Gly Val Leu Val Pro Pro Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn			
85 90 95			
Pro His Thr Asn Phe Thr Val Pro Thr Val Trp Gly Ser Thr Val Gln			
100 105 110			
Val Ser Trp Leu Ala Leu Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala			
115 120 125			

Asp Lys Ile His Leu Ala Ser Glu Arg Gly Ala Ser Gly Ala Val Ile
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 Phe Asn Phe Pro Gly Thr Arg Asn Glu Val Ile Pro Met Ser His Pro
 145 150 155 160
 Gly Ala Gly Asp Ile Val Ala Ile Met Ile Gly Asn Leu Lys Gly Thr
 165 170 175
 Lys Ile Leu Gln Ser Ile Gln Arg Gly Ile Gln Val Thr Met Val Ile
 180 185 190
 Glu Val Gly Lys Lys His Gly Pro Trp Val Asn His Tyr Ser Ile Phe
 195 200 205
 Phe Val Ser Val Ser Phe Phe Ile Ile Thr Ala Ala Thr Val Gly Tyr
 210 215 220
 Phe Ile Phe Tyr Ser Ala Arg Arg Leu Arg Asn Ala Arg Ala Gln Ser
 225 230 235 240
 Arg Lys Gln Arg Gln Leu Lys Ala Asp Ala Lys Lys Ala Ile Gly Lys
 245 250 255
 Leu Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro Asp
 260 265 270
 Gly Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp Leu
 275 280 285
 Val Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val Asp
 290 295 300
 Pro Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp Ile
 305 310 315 320
 Leu Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val Ser
 325 330 335
 Leu Gln Val Pro Val Ser Asn Glu Ala Ser Asn Thr Ala Ser Pro His
 340 345 350
 Glu Glu Asp Ser Arg Ser Glu Thr Ala Ser Ser Gly Tyr Ala Ser Val
 355 360 365
 Gln Gly Ala Asp Glu Pro Pro Leu Glu Glu His Ala Gln Ser Ala Asn
 370 375 380
 Glu Asn Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val Asp
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 Asp Gln Glu Ala Ala Val Arg Glu Ile Lys Ser
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 cctggctcgc acgtagctcg cagctcccca gtctcactoc attccttccc cacctggcgc 180
 gcacctgctc aagaccaggg tctgccaag cgctaggagg gcgcgtgcca gggcgctag 240
 ggaactgcgg agcgcgcgcg cc atg ggg ccg cct ggg gcc ggg gtc tcc 292

Met Gly Pro Pro Pro Gly Ala Gly Val Ser
1 5 10

tgc cgc ggt ggc tgc ggc ttt tcc aga ttg ctg gca tgg tgc ttc ctg Cys Arg Gly Gly Cys Gly Phe Ser Arg Leu Leu Ala Trp Cys Phe Leu	340
15 20 25	
ctg gcc ctg agt ccg cag gca ccc ggt tcc cgg ggg gct gaa gca gtg Leu Ala Leu Ser Pro Gln Ala Pro Gly Ser Arg Gly Ala Glu Ala Val	388
30 35 40	
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45 50 55	
aac cgt acg gtg tgg gag ctg agc gag gag ggc gtg tac ggc cag gac Asn Arg Thr Val Trp Glu Leu Ser Glu Glu Gly Val Tyr Gly Gln Asp	484
60 65 70	
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75 80 85 90	
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95 100 105	
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110 115 120	
ggc ggg ggc tgc acc ttc gca gac aag atc cat ctg gct tat gag aga Gly Gly Gly Cys Thr Phe Ala Asp Lys Ile His Leu Ala Tyr Glu Arg	676
125 130 135	
tgg gcg tct gga gcc gtc atc ttt aac ttc ccc ggg acc cgc aat gag Trp Ala Ser Gly Ala Val Ile Phe Asn Phe Pro Gly Thr Arg Asn Glu	724
140 145 150	
gtc atc ccc atg tct cac ccg ggt gca gta gac att gtt gca atc atg Val Ile Pro Met Ser His Pro Gly Ala Val Asp Ile Val Ala Ile Met	772
155 160 165 170	
atc ggc aat ctg aaa ggc aca aaa att ctg caa tct att caa aga ggc Ile Gly Asn Leu Lys Gly Thr Lys Ile Leu Gln Ser Ile Gln Arg Gly	820
175 180 185	
ata caa gtg aca atg gtc ata gaa gta ggg aaa aaa cat ggc cct tgg Ile Gln Val Thr Met Val Ile Glu Val Gly Lys Lys His Gly Pro Trp	868
190 195 200	
gtg aat cac tat tca att ttt ttc gtt tct gtg tcc ttt ttt att att Val Asn His Tyr Ser Ile Phe Phe Val Ser Val Ser Phe Phe Ile Ile	916
205 210 215	
acg gcg gca act gtg ggc tat ttt atc ttt tat tct gct cga agg cta Thr Ala Ala Thr Val Gly Tyr Phe Ile Phe Tyr Ser Ala Arg Arg Leu	964
220 225 230	

cgg aat gca aga gct caa agc agg aag cag agg caa tta aag gca gat	1012
Arg Asn Ala Arg Ala Gln Ser Arg Lys Gln Arg Gln Leu Lys Ala Asp	
235 240 245 250	
gct aaa aaa gct att gga agg ctt caa cta cgc aca ctg aaa caa gga	1060
Ala Lys Lys Ala Ile Gly Arg Leu Gln Leu Arg Thr Leu Lys Gln Gly	
255 260 265	
gac aag gaa att ggc cct gat gga gat agt tgt gct gtg tgc att gaa	1108
Asp Lys Glu Ile Gly Pro Asp Gly Asp Ser Cys Ala Val Cys Ile Glu	
270 275 280	
ttg tat aaa cca aat gat ttg gta cgc atc tta acg tgc aac cat att	1156
Leu Tyr Lys Pro Asn Asp Leu Val Arg Ile Leu Thr Cys Asn His Ile	
285 290 295	
ttc cat aag aca tgt gtt gac cca tgg ctg tta aaa cac aag act tgc	1204
Phe His Lys Thr Cys Val Asp Pro Trp Leu Leu Lys His Lys Thr Cys	
300 305 310	
ccc atg tgc aaa tgt gac ata ctc aaa gct ttg gga att gag gtg gat	1252
Pro Met Cys Lys Cys Asp Ile Leu Lys Ala Leu Gly Ile Glu Val Asp	
315 320 325 330	
gtt gaa gat gga tca gtg tct tta caa gtc cct gta tcc aat gaa ata	1300
Val Glu Asp Gly Ser Val Ser Leu Gln Val Pro Val Ser Asn Glu Ile	
335 340 345	
tct aat agt gcc tcc tcc cat gaa gag gat aat cgc agc gag acc gca	1348
Ser Asn Ser Ala Ser Ser His Glu Glu Asp Asn Arg Ser Glu Thr Ala	
350 355 360	
tca tct gga tat gct tca gta cag gga aca gat gaa ccg cct ctg gag	1396
Ser Ser Gly Tyr Ala Ser Val Gln Gly Thr Asp Glu Pro Pro Leu Glu	
365 370 375	
gaa cac gtg cag tca aca aat gaa agt cta cag ctg gta aac cat gaa	1444
Glu His Val Gln Ser Thr Asn Glu Ser Leu Gln Leu Val Asn His Glu	
380 385 390	
gca aat tct gtg gca gtg gat gtt att cct cat gtn gac aac cca acc	1492
Ala Asn Ser Val Ala Val Asp Val Ile Pro His Val Asp Asn Pro Thr	
395 400 405 410	
ttt gaa gaa gac gaa act cct aat caa gag act gct gtt cga gaa att	1540
Phe Glu Glu Asp Glu Thr Pro Asn Gln Glu Thr Ala Val Arg Glu Ile	
415 420 425	
aaa tct t aaaatctgtg taaatagaaa acttgaacca ttagtaataa cagaactgcc	1597
Lys Ser	
aatcagggcc tagtttctat taataaattg gataaattta ataaaataag agtgatactg	1657
aaagtgtcga gatgactaat attatgctat agttaaaatg gcttaaaaat atttaacctg	1717
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[illegible]

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Ala	Pro	Gly	Ser	Arg	Gly	Ala	Glu	Ala	Val	Trp	Thr	Ala	Tyr	Leu	Asn
Val	Ser	Trp	Arg	Val	Pro	His	Thr	Gly	Val	Asn	Arg	Thr	Val	Trp	Glu
Leu	Ser	Glu	Glu	Gly	Val	Tyr	Gly	Gln	Asp	Ser	Pro	Leu	Glu	Pro	Val
Ala	Gly	Val	Leu	Val	Pro	Pro	Asp	Gly	Pro	Gly	Ala	Leu	Asn	Ala	Cys
Asn	Pro	His	Thr	Asn	Phe	Thr	Val	Pro	Thr	Val	Trp	Gly	Ser	Thr	Val
Gln	Val	Ser	Trp	Leu	Ala	Leu	Ile	Gln	Arg	Gly	Gly	Gly	Cys	Thr	Phe
Ala	Asp	Lys	Ile	His	Leu	Ala	Tyr	Glu	Arg	Trp	Ala	Ser	Gly	Ala	Val
Ile	Phe	Asn	Phe	Pro	Gly	Thr	Arg	Asn	Glu	Val	Ile	Pro	Met	Ser	His
Pro	Gly	Ala	Val	Asp	Ile	Val	Ala	Ile	Met	Ile	Gly	Asn	Leu	Lys	Gly
Thr	Lys	Ile	Leu	Gln	Ser	Ile	Gln	Arg	Gly	Ile	Gln	Val	Thr	Met	Val
Ile	Glu	Val	Gly	Lys	Lys	His	Gly	Pro	Trp	Val	Asn	His	Tyr	Ser	Ile
Phe	Phe	Val	Ser	Val	Ser	Phe	Phe	Ile	Ile	Thr	Ala	Ala	Thr	Val	Gly
Tyr	Phe	Ile	Phe	Tyr	Ser	Ala	Arg	Arg	Leu	Arg	Asn	Ala	Arg	Ala	Gln
Ser	Arg	Lys	Gln	Arg	Gln	Leu	Lys	Ala	Asp	Ala	Lys	Lys	Ala	Ile	Gly
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Asp	Gly	Asp	Ser	Cys	Ala	Val	Cys	Ile	Glu	Leu	Tyr	Lys	Pro	Asn	Asp
Leu	Val	Arg	Ile	Leu	Thr	Cys	Asn	His	Ile	Phe	His	Lys	Thr	Cys	Val
Asp	Pro	Trp	Leu	Leu	Lys	His	Lys	Thr	Cys	Pro	Met	Cys	Lys	Cys	Asp
Ile	Leu	Lys	Ala	Leu	Gly	Ile	Glu	Val	Asp	Val	Glu	Asp	Gly	Ser	Val
Ser	Leu	Gln	Val	Pro	Val	Ser	Asn	Glu	Ile	Ser	Asn	Ser	Ala	Ser	Ser
His	Glu	Glu	Asp	Asn	Arg	Ser	Glu	Thr	Ala	Ser	Ser	Gly	Tyr	Ala	Ser
Val	Gln	Gly	Thr	Asp	Glu	Pro	Pro	Leu	Glu	Glu	His	Val	Gln	Ser	Thr
Asn	Glu	Ser	Leu	Gln	Leu	Val	Asn	His	Glu	Ala	Asn	Ser	Val	Ala	Val
Asp	Val	Ile	Pro	His	Val	Asp	Asn	Pro	Thr	Phe	Glu	Glu	Asp	Glu	Thr
Pro	Asn	Gln	Glu	Thr	Ala	Val	Arg	Glu	Ile	Lys	Ser				

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